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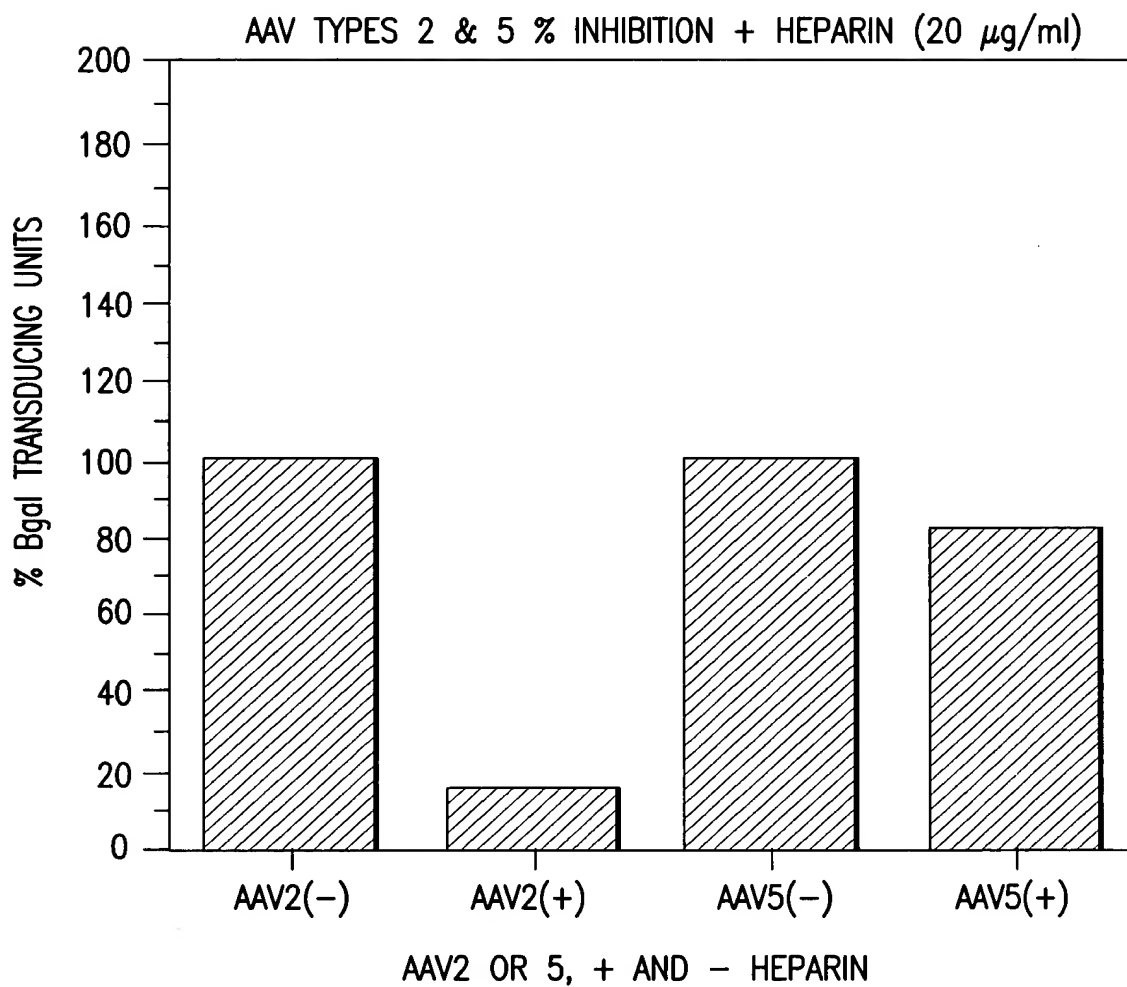
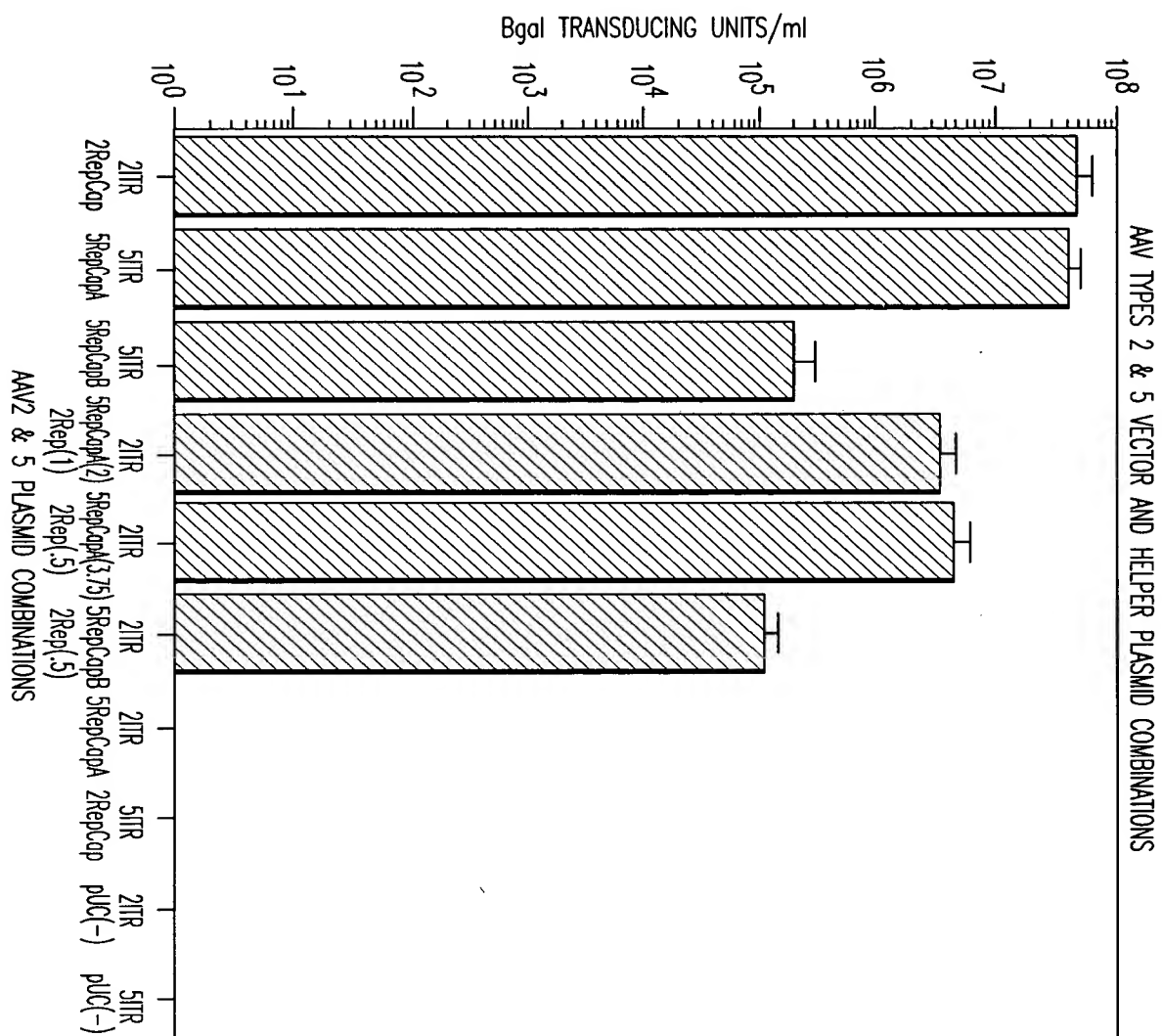


FIG.1

FIG. 2



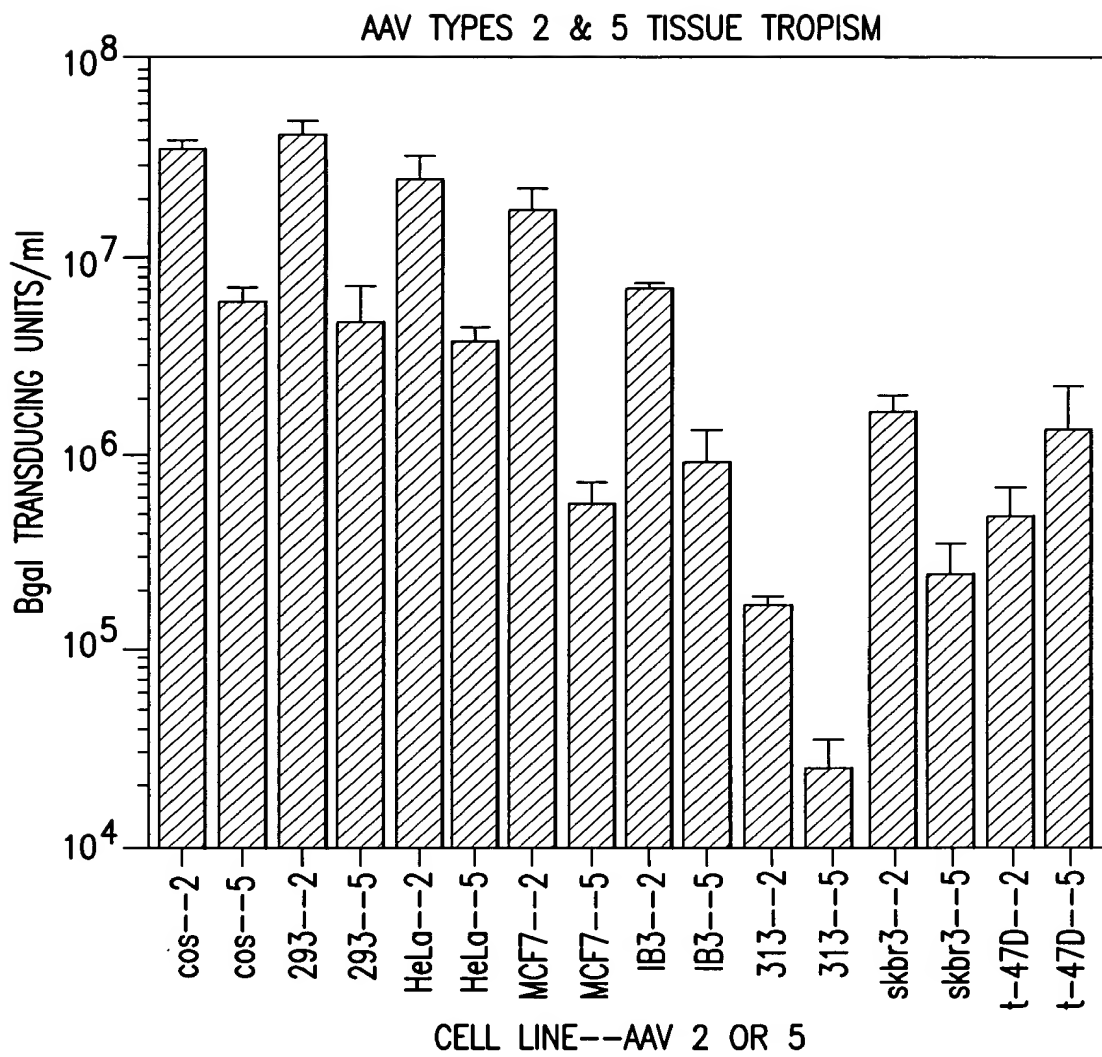


FIG.3

ALIGNMENT OF TWO NUCLEOTIDE SEQUENCES.

THE TWO SEQUENCES TO BE ALIGNED ARE:

AAV2CG.

TOTAL NUMBER OF BASES: 4679.

AAV5CG.TOTAL NUMBER OF BASES: 4652.

OPEN GAP COST: 10

UNIT GAP COST: 12

THE CHARACTER TO SHOW THAT TWO ALIGNED RESIDUES ARE IDENTICAL IS ":"

```
AAV2CG - TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGA-----GGCCGGGCGA -48
      : : : :::: :   :::: ::::::::::: ::      :: :: :
AAV5CG - TGGCACTCTCCCCCTGTGCGGTTGCTCGCTCGCTGGCTCGTTTGGGGGGGTGG -55

AAV2CG - C----CAAAGGTC-GCCCCACGCCCCGGGCTTTGCCCCG-GCGGCCTCA----- -90
      :   :::: : :: :::: : : :: :: :::: : : :: :
AAV5CG - CAGCTCAAAGAGCTGCCAGACGACGGCCCTCTGGCCGTCGCCCCCCTAAACGAGC -110

AAV2CG - --GTGAGCGAGCGAGCGCG-CAGAGAGG-GAGTGGCCAACTCCATCACTAGGGGT -141
      : ::::::::::: :::: :: : :: :::: : :::: : ::::
AAV5CG - CAGCGAGCGAGCGAACGCGACAGGGGGGAGAGTGCCCACTCTCAAGCAAGGGGG -165

AAV2CG - TCCTGGAGGG-GTGGAGTCGTGACG-TGAATTACGTCATAGGGTTAGGGAGGTCC -194
      : :: : : :::: :::: : : : : : : : : : : :
AAV5CG - TTTTGTAAGCAGTGATGTCATAATGATGTAATGCTTATTGTCACGCGATAGTTAA -220

AAV2CG - TGTATTAGAGGTCACGTGA-GTGTTTTGCGACATTTTGGGACACC-----ATGT -242
      :: :::: :::: :::: :::::::::: :: :: : : : ::
AAV5CG - TG-ATTAACAGTCATGTGATGTGTTTTATCCAATAGGAAGAAAGCGCGCGTATGA -274

AAV2CG - GGTACGCT-----GGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCAT -288
      : : : : ::::: :::: :::::::::: : : : : : : :
AAV5CG - GTTCTCGCGAGACTTCCGGGGTATAAAGACCGAGTGAACGAGCCCGC-CGCCAT -328

AAV2CG - T-TTGAAGCGGGAG-GTTTGAACGCGCA-GCCGCCATGCCGGGGTTTTACGAGAT -340
      : :: : :::: : : : : : : : ::::: : : : : :
AAV5CG - TCTTTGCTCTGCACTGCTAGAGGACCTCGCTGCCATGGCTACCTTCTATGAAGT -383
```

FIG.4A

AAV2CG - TGTGATTAAGGTCCCCAGCGACCTTGACGGGCATCTGCCCCGGCATTCTGACAGC -395
 : : : : : : : : : : :
 AAV5CG - CATTGTTGCGGTCCCATTGACGTGGAGGAACATCTGCCTGGAATTTCTGACAGC -438

 AAV2CG - TTTGTGAACTGGGTGGCCGAGAAGGAATGGGAGTTGCCGCCAGATTCTGACATGG -450
 : : : : : : : : : : :
 AAV5CG - TTTGTGGACTGGGTAACTGGTCAAATTTGGGAGCTGCCTCCAGAGTCAGATTAA -493

 AAV2CG - ATCTGAATCTGATTGAGCAGGCACCCCTGACCGTGGCCGAGAAGCTGCAGCGCGA -505
 : : : : : : : : : : : :
 AAV5CG - ATTTGACTCTGGTTGAACAGCCTCAGTTGACGGTGGCTGATAGAATTCGCCGCGT -548

 AAV2CG - CTTTCTGACGGAATGGCGCCGTGTGAGTAAGGCCCCGGAGGCCCTTTTCTTTGTG -560
 : : : : : : : : : : : :
 AAV5CG - GTTCCTGTACGAGTGAACAAATTTCCAAG---CAGGAGTCCAAATCTTTGTG -600

 AAV2CG - CAATTTGAGAAGGGAGAGAGCTACTTCCACATGCACGTGCTCGTGGAAACCACCG -615
 : : : : : : : : : : : :
 AAV5CG - CAGTTTGAAAAGGGATCTGAATATTTTCATCTGCACACGCTTGTGGAGACCTCCG -655

 AAV2CG - GGGTGAAATCCATGGTTTTGGGACGTTTCCTGAGTCAGATTCGCGAAAACTGAT -670
 : : : : : : : : : : : :
 AAV5CG - GCATCTCTTCCATGGTCCTCGGCCGCTACGTGAGTCAGATTCGCGCCCAGCTGGT -710

 AAV2CG - TCAGAGAATTTACCGCGGGATCGAGCCGACTTTGCCAAACTGGTTCGCGGTCACA -725
 : : : : : : : : : : : :
 AAV5CG - GAAAGTGGTCTTCCAGGGAATTGAACCCAGATCAACGACTGGGTGCCATCACC -765

 AAV2CG - AAGACCAGAAATGGCGCCGGAGGCGGGAACAAGGTGGTGGATGAGTGCTACATCC -780
 : : : : : : : : : : : :
 AAV5CG - AAGGTAAAGAAGGGC---GGAGCC---AATAAGGTGGTGGATTCTGGGTATATTC -814

 AAV2CG - CCAATTACTTGCTCCCCAAAACCCAGCCTGAGCTCCAGTGGGCGTGGACTAATAT -835
 : : : : : : : : : : : :
 AAV5CG - CCGCCTACCTGCTGCCGAAGGTCCAACCGGAGCTTCAGTGGGCGTGGACAAACCT -869

 AAV2CG - GGAACAGTATTTAAGCGCCTGTTTGAATCTCACGGAGCGTAAACGGTTGGTGGCG -890
 : : : : : : : : : : : :
 AAV5CG - GGACGAGTATAAATTGGCCGCCCTGAATCTGGAGGAGCGCAAACGGCTCGTCGCG -924

FIG.4B

AAV2CG - CAGCATCTGACGCACGTGTGCGCAGACGCAGGAGCAGAACAAAGAGAATCAGAATC -945
 :
 AAV5CG - CAGTTTCTGGCAGAATCCTCGCAG-CGCTCG--CAGGAGGCGGCTTCGCAGCGTG -976

 AAV2CG - CCAATTCTGATGCGCCGGTGATCAGATCAAAAACTTCAGCCAGGTACATGGAGCT -1000
 :
 AAV5CG - AGTTCTCGGCTGACCCGGTCATCAAAAGCAAGACTTCCCAGAAATACATGGCGCT -1031

 AAV2CG - GGTGCGGTGGCTCGTGGACAAGGGGATTACCTCGGAGAAGCAGTGGATCCAGGAG -1055
 :
 AAV5CG - CGTCAACTGGCTCGTGGAGCACGGCATCACTTCCGAGAAGCAGTGGATCCAGGAA -1086

 AAV2CG - GACCAGGCCCTCATACATCTCCTTCAATGCGGCCTCCAACTCGCGGTCCCAAATCA -1110
 :
 AAV5CG - AATCAGGAGAGCTACCTCTCCTTCAACTCCACCGGCAACTCTCGGAGCCAGATCA -1141

 AAV2CG - AGGCTGCCTTGGACAATGCGGGAAAGATTATGAGCCTGACTAAAACCGCCCCCGA -1165
 :
 AAV5CG - AGGCCGCGCTCGACAACGCGACCAAAATTATGAGTCTGACAAAAAGCGCGGTGGA -1196

 AAV2CG - CTACCTGGTGGGCCAGCAGCCCGTG-GAGGACATTTCCAGCAATCGGATTTATAA -1219
 :
 AAV5CG - CTACCTCGTGGGG-AGCTCCGTTCCCGAGGACATTTCAAAAAACAGAATCTGGCA -1250

 AAV2CG - AATTTTGAACTAAACGGGTACGATCCCCAATATGCGGGCTTCCGTCTTTCTGGGA -1274
 :
 AAV5CG - AATTTTGTGAGATGAATGGCTACGACCCGGCCTACGCGGGATCCATCCTCTACGGC -1305

 AAV2CG - TGGGCCACGAAAAAGTTGCGGCAAGAGGAACACCATCTGGCTGTTTGGGCCTGCAA -1329
 :
 AAV5CG - TGGTGTGAGCGCTCCTTCAACAAGAGGAACACCGTCTGGCTCTACGGACCCGCCA -1360

 AAV2CG - CTACCGGGAAGACCAACATCGCGGAGGCCATAGCCCACACTGTGCCCTTCTACGG -1384
 :
 AAV5CG - CGACCGGCAAGACCAACATCGCGGAGGCCATCGCCACACTGTGCCCTTTTACGG -1415

 AAV2CG - GTGCGTAAACTGGACCAATGAGAACTTTCCCTTCAACGACTGTGTGACAAGATG -1439
 :
 AAV5CG - CTGCGTGAACCTGGACCAATGAAAACTTTCCCTTTAATGACTGTGTGGACAAAATG -1470

FIG.4C

AAV2CG	- GTGATCTGGTGGGAGGAGGGGAAGATGACCCCAAGGTCTGGAGTCGGGCCAAAG -1494 : : :::::::::::::::::::: : : : : :
AAV5CG	- CTCATTTGGTGGGAGGAGGGAAAAGATGACCAACAAGGTGGTTGAATCCGCCAAGG -1525
AAV2CG	- CCATTCTCGGAGGAAGCAAGGTGCGCGTGACCAGAAATGCAAGTCCTCGGCCCA -1549 ::: : : : : :::::::::: : : : : : :
AAV5CG	- CCATCCTGGGGGGCTCAAAGGTGCGGGTCGATCAGAAATGTAAATCCTCTGTTCA -1580
AAV2CG	- GATAGACCCGACTCCCCTGATCGTCACCTCCAACACCAACATGTGCGCCGTGATT -1604 : : : : : : : : : : : : : : : : : : :
AAV5CG	- AATTGATTCTACCCCTGTCAATTGTAAC TTCCAATACAAACATGTGTGTGGTGGTG -1635
AAV2CG	- GACGGGAACTCAACGACCTTCGAACACCAGCAGCCGTTGCAAGACCGGATGTTCA -1659 : : :::: : : :::::::::: : : : : : : :
AAV5CG	- GATGGGAATTCCACGACCTTTGAACACCAGCAGCCGCTGGAGGACCGCATGTTCA -1690
AAV2CG	- AATTTGAACTCACCCGCCGTCTGGATCATGACTTTGGGAAGGTCACCAAGCAGGA -1714 :::::::::::: : : : : : : : : : : : : :
AAV5CG	- AATTTGAACTGACTAAGCGGCTCCCGCCAGATTTTGGCAAGATTACTAAGCAGGA -1745
AAV2CG	- AGTCAAAGACTTTTTCCGGTGGGCAAAGGATCACGTGGTTGAGGTGGAGCATGAA -1769 ::: : : : : :::::::::: : : : : : : : :
AAV5CG	- AGTCAAGGACTTTTTTGCTTGGGCAAAGGTCAATCAGGTGCCGGTGA CT CACGAG -1800
AAV2CG	- TTCTACGTCAAAAAGGG--TGGAGCCAAGAAAAGACCCGCCCCCAGTGACGCAGA -1822 : : : : : : : : : : : : : : : :
AAV5CG	- TTTAAAGTTCCCAGGGAATTGGCGGGA ACT AAAGGGGCG-----GAGAAATCTC -1849
AAV2CG	- TATAAGTGAGCCCAAACGGGTGCGCGAGTCAGTTGCGCAGCCATCGACGTCAGAC -1877 : : : : : : : : : : : : : : : :
AAV5CG	- TAAAAC---GCCCACT-GGGTGA-CGTACCAATACT-AGCTATAAAAGTCTGGA -1898
AAV2CG	- GCGGAAGCTTCGATCAACTACGCAGACAGGTACCAAAACAAAT-GTTCTCGTCAC -1931 : : : : : : : : : : : : : : : :
AAV5CG	- G---AAGC--GGGCCAGGCTCTCATTT-GTTCCCGAGACGCCTCGCAGTTCAGAC -1947
AAV2CG	- GTGGGCATGAATCT-GATGCTGTTTCCCTGCAGACAATGCGAGAGAATGAATCAG -1985 : : : : : : : : : : : : : : : :
AAV5CG	- GTGACTGTTGATCCCGCTCCTCTGCGACCGCTCA-ATTGGAATTC AAGGTAT--G -1999

FIG. 4D

AAV2CG - AATTCAAATATCTGCTTCACTCACGGACAGAAAGACTGTTTAGAGTGCTTTCCCG -2040
 :
 AAV5CG - ATTGCAAATG--TGA CT-A-TCATGGCTCAATTTGACA----ACATTTCTAACAAA -2046

 AAV2CG - TGTCA-GAATCTCAACCCGTTTCTGTCGTCAAAAAGGC--GTATCAGAACTGTG -2092
 :
 AAV5CG - TGTGATGAATGTGAATATTTGAATCGGGGCAAAAATGGATGTATCTGTCTACAATG -2101

 AAV2CG - CTACATTCA-TCATAT----CATGGGAAAGGTGCCAGACGCTTGCACTGCCTGCCG -2142
 :
 AAV5CG - TAACTCACTGTCAAATTTGTCATGGGATTCCCCCTGGGAAAAGGAAAAC TTG-- -2154

 AAV2CG - ATCTGGTCAATGTGGATTTGGATGACTGCATCTTTGAACAATAAATGATTTAAAT -2197
 :
 AAV5CG - -TCAGATTT-TGGGGATTTTGACGATGCCAATAAAGAACAGTAAATAAAGCGAGT -2207

 AAV2CG - CAGGTATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGA -2252
 :
 AAV5CG - -AGTCATGTCTTTTGTGATCACCTCCAGATTGGTTGGAAGAAGTTGG---TGA -2258

 AAV2CG - AGGAATAAGACAGTGGTGGAAAGCTCAAACCTGGCCCACCACCACCAAAGCCCGCA -2307
 :
 AAV5CG - AGGTCTTCGCCGAGTTTTGGGGCCTTGAAGCGGGCCCACCGAAACCAAACCCAAT -2313

 AAV2CG - GAGCGGCATAAGGACGACAGCAGGGGTCTTGTGCTTCCTGGGTACAAGTACCTCG -2362
 :
 AAV5CG - CAGCAGCATCAAGATCAAGCCCGTGGTCTTGTGCTGCCTGGTTATAACTATCTCG -2368

 AAV2CG - GACCCCTTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCAGACGCCGCGGC -2417
 :
 AAV5CG - GACCCGGAACCGTCTCGATCGAGGAGAGCCTGTCAACAGGGCAGACGAGGTCTCG -2423

 AAV2CG - CCTCGAGCACGACAAAGCCTACGACCGGCAGCTCGACAGCGGAGACAACCCGTAC -2472
 :
 AAV5CG - GCGAGAGCACGACATCTCGTACAACGAGCAGCTTGAGGCGGGAGACAACCCCTAC -2478

 AAV2CG - CTCAAGTACAACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAAGATACGT -2527
 :
 AAV5CG - CTCAAGTACAACCACGCCGACGCGGAGTTTCAGGAGAAGCTCGCCGACGACACAT -2533

FIG.4E

AAV2CG - TTTCACCACGTGACTGGCAAAGACTCATCAACAACAACTGGGGATTCCGACCCAA -3128
 :: :: :: :::::::::: :::: :::::
 AAV5CG - GGAGCCCCCGAGACTGGCAAAGACTCATCAACAACCTACTGGGGCTTCAGACCCCG -3110

 AAV2CG - GAGACTCAACTTCAAGCTCTTTAACATTCAAGTCAAAGAGGTCACGCAGAATGAC -3183
 : ::: ::: ::: ::::::::::::::::::::::::::::::::: : : :::
 AAV5CG - GTCCCTCAGAGTCAAAATCTTCAACATTCAAGTCAAAGAGGTCACGGTGCAGGAC -3165

 AAV2CG - GGTACGACGACGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGACT -3238
 :: :: :: :: :: ::::: ::::: :::: :::: :: :: ::::::::::: :::
 AAV5CG - TCCACCACCACCATCGCCAACAACCTCACCTCCACCGTCCAAGTGTTTACGGACG -3220

 AAV2CG - CGGAGTACCAGCTCCCGTACGTCCTCGGGCTCGGCGCATCAAGGATGCCTCCCGCC -3293
 :: ::::::::::: :: ::::: ::::: : : : ::::::::::: :::: :
 AAV5CG - ACGACTACCAGCTGCCCTACGTCGTGCGCAACGGGACCGAGGGATGCCTGCCGGC -3275

 AAV2CG - GTTCCCAGCAGACGTCTTCATGGTGCCACAGTATGGATACCTCACCTGAACAAC -3348
 ::::: : : ::::: : : ::::: ::::: :: :::: : : ::::: :
 AAV5CG - CTTCCCTCCGCAGGTCTTTACGCTGCCGAGTACGGTTACGCGACGCTGAACCGC -3330

 AAV2CG - GGGAGT-CAGGCAGTAGGAC---GCTCTTCA--TTTTACTGCCTGGAGTACTTTC -3397
 : : ::: : : :: : :: : : ::::: :::::::::::
 AAV5CG - GACAACACAGAAAATCCCAACCGAGAGGAGCAGCTTCTTCTGCCTAGAGTACTTTC -3385

 AAV2CG - CTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGCTACACTTTTGAGGA -3452
 : :::::::::: : :: :: ::::::::::: :: : ::::: :::::::::::
 AAV5CG - CCAGCAAGATGCTGAGAACGGGCAACAACTTTGAGTTTACCTACAACTTTGAGGA -3440

 AAV2CG - CGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAAT -3507
 :: :: ::::: ::::: ::::: ::::: ::::: :::: : : :::: :
 AAV5CG - GGTGCCCTTCCACTCCAGCTTCGCTCCCAGTCAGAACCTGTTCAAGCTGGCCAAC -3495

 AAV2CG - CCTCTCATCGACCAGTACCTGTATTACTT---GAGCAGAACAAACACTC----- -3553
 :: :: : ::::::::::: ::::: ::::: ::::: :: ::::: :::::
 AAV5CG - CCGCTGGTGGACCACTACTTGTACCGCTTCGTGAGCACAAATAACACTGGCGGAG -3550

 AAV2CG - -CAAGTGAACCACCAC---GCAGTCA-AGGCTTCAGTT--TTCTCAGGCCGGAG -3601
 : :: : ::::: : : : : : : : : : : : : : : : : : :
 AAV5CG - TCCAGTTCAACAAGAACCTGGCCGGGAGATACGCCAACACCTACAAAACTGGTT -3605

FIG.4G

AAV2CG - ACACCCCGGTACCTGCGAATCCTTCGACCACCTTCAGTG-CGGCAAAGTTTGCTT -4204
 :
 AAV5CG - ACACGCCTGTGCCCCGAAATA--TC-ACCAGCTTCTCGGACGTGCCCGTCAGCAG -4181

 AAV2CG - CCTTCATCACACAGTACTCCACGGGACAGGTCAGCGTGGAGATCGAGTGGGAGCT -4259
 :
 AAV5CG - C-TTCATCACCCAGTACAGCACCGGGCAGGTCACCGTGGAGATGGAGTGGGAGCT -4235

 AAV2CG - GCAGAAGGAAAACAGCAAACGCTGGAATCCCGAAATTCAGTACACTTCCAACACTAC -4314
 :
 AAV5CG - CAAGAAGGAAAACCTCCAAGAGGTGGAACCCAGAGATCCAGTACACAAACAACACTAC -4290

 AAV2CG - AACAAGTCTGTTAATGTGGACTTTACTGTGGACACTAATGGCGTGTATTTCAGAGC -4369
 :
 AAV5CG - AACGACCCCCAGTTTGTGGACTTTGCCCCGACAGCACCGGGGA--ATACAGAAC -4343

 AAV2CG - CTC--GCCCCATTGGCACCAGATACCTGACTCGTAATCTGTAAT--TGCTTGT- -4418
 :
 AAV5CG - CACCAGACCTATCGGAACCCGATACCTTACCCGACCCCTTAACCCATTTCATGTC -4398

 AAV2CG - ---TAA--TCAATAAACCGTTTAATTCGTTTCAGTTGAACTTTGG-TCTCTGCGT -4467
 :
 AAV5CG - GCATACCCTCAATAAACCGTGTA-TTCGTGTCAGTAAAATACTGCCTCTTGTGGT -4452

 AAV2CG - ATTTCTTTCT-TATCTAGTTTCCATGGCTACGTAGATAAGTAGCATGGCGGGTTA -4521
 :
 AAV5CG - CATTCAATGAATAACAGCTTACAACATCTACAAAACCTCCTTGCTTGA-GAGTGT -4506

 AAV2CG - ATCATTAAC TACAAGGAACCCCTAGTGATGGAGTTGGCCACTCCCTC-TCTGCGC -4575
 :
 AAV5CG - GGC ACT--CTCCCC---CCTGTCGCGTTCGC-TCGCTCGCTGGCTCGTTTGGGG -4554

 AAV2CG - GCTCGCTCGCTCACTGAG--GCCGGGGACCAAAGGTCGCCCCGACGCCCGGGCTT -4628
 :
 AAV5CG - GGGTGGCAGCTCAAAGAGCTGCCAGACGACGGCCCTCTGGCCGTCGCCCC----- -4604

 AAV2CG - TGCCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAA -4679
 :
 AAV5CG - --CCCAAACGAGC-CAGCGAGCGAGCGAACGCGACAGGGGGGAGAGTGCCA- -4652

FIG.4I

Identity : 3013 (64.77%)
Number of gaps inserted in AAV2CG: 43
Number of gaps inserted in AAV5CG: 63

FIG.4J

ALIGNMENT OF TWO PROTEIN SEQUENCES.

The two sequences to be aligned are:

AAV2VPI.

DE VPI

OS AAV2

Total number of residues: 735.

AAV5VP1.

DE AAV5VP1

OS AAV5VP1

Total number of residues: 724. 2101-4272

Comparison matrix : Structure-genetic matrix.

Open gap cost: 8

Unit gap cost: 5

The character to show that two aligned residues are identical is ':'

The character to show that two aligned residues are similar is '.'

Amino acids said to be 'similar' are: A,S,T; D,E; N,Q; R,K; I,L,M,V;
F,Y,W

AAV2VPI - MAADGYLPDWLEDTLSEGIQWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGP -55

:. : . . . : : : : :

AAV5VP1 - MSFVDHPPDWLEE-VGEGLREFLGLEAGPPKPKPNQQHQDQARGLVLPGYNYLGP -54

AAV2VPI - FNGLDKGEPVNEADAAALEHDKAYDRQLDSCGNPYLKYNHADADEFQERLKEDTSF -110

: : : : : : : :

AAV5VP1 - GNGLDRGEPVNRADDEVAREHDISYNEQLEAGDNPYLKYNHADADEFQEKLADDTSF -109

AAV2VPI - GGNLGRAVFQAKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEPDSSSGTGKAGQQ -165

: : : : : : : : . : . :

AAV5VP1 - GGNLGKAVFQAKKRVLEPFGLVEEGAKTAPTGKRIDDHFPKR--KKARTEEDSKP -162

AAV2VPI - PARKRLNFGQTGDADSVDPDPQLGQPPAAPSGLGTNTMATGSGAPMADNNEGADG -220

. . . : : : : : : : :

AAV5VP1 - STS-----SDAEAGPSGSQQLQIPAQPASSLGADTMSAGGGGPLGDNNQCADG -210

FIG.5A

Identity: 421 (58.15%)
Similarity: 63 (8.70%)
Number of gaps inserted in AAV2VP1: 3
Number of gaps inserted in AAV5VP1: 5

FIG.5C

ALIGNMENT OF TWO PROTEIN SEQUENCES.

The two sequences to be aligned are:

REP78.

DE REP78

OS AAV

Total number of residues: 621.

AAV5REP.

DE REP

OS AAV5

Total number of residues: 610.

Comparison matrix: Structure-genetic matrix.

Open gap cost: 8

Unit gap cost: 5

The character to show that two aligned residues are identical is ':'

The character to show that two aligned residues are similar is '.'

Amino acids said to be similar are: A,S,T; D,E; N,Q; R,K; I,L,M,V; F,Y,W

```
REP78   - MPGFYEIVIKVPSDL DGHLPGISDSFVNWVAEK EWELPPDSMDLNLIEQAPLTV -55
          : ::::: : : : : : : : : : : : : : : : : : : : : : : : : : :
AAV5REP - MATFYEVIVRVPFDVEEHLPGISDSFVDWVTGQIWELPPESDLNLT LVEQPQLTV -55

REP78   - AEKLQRDFLTEWRRVSKAPEALFFVQFEKGESYFHMHVLVETTGVKSMVLGRFLS -110
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AAV5REP - ADRIIRRVFLEWNKFSKRQ-ESKFFVQFEKGSEYFHLHTLVETSGISSMVLGRYVS -109

REP78   - QIREKLIQRIYRGIEPTLPNWEAVTKTRNGAGGCKNVVDECYIPNYLLPKTQPEL -165
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AAV5REP - QIRAQLVKVVFQGI EPQINDWVAITKVKKG--GANKVVDSGYIPAYLLPKVQPEL -162

REP78   - QWAWTNMEQYLSACLNLTERKRLVAQHLTHVSQTQE QNKENQNPNSDAPVIRSKT -220
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AAV5REP - QWAWTNLDEYKLAALNLEERKRLVAQFLA-ESSQRSQEAASQREFSADPVIKSKT -216

REP78   - SARYMELVGWLVDKGITSEKQW IQEDQASYISFNAASNRSQIKAALDNAGKIMS -275
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AAV5REP - SQKYMALVNWLVEHGITSEKQW IQENQESYLSFNSTGNSRSQIKAALDNATKIMS -271
```

FIG.6A

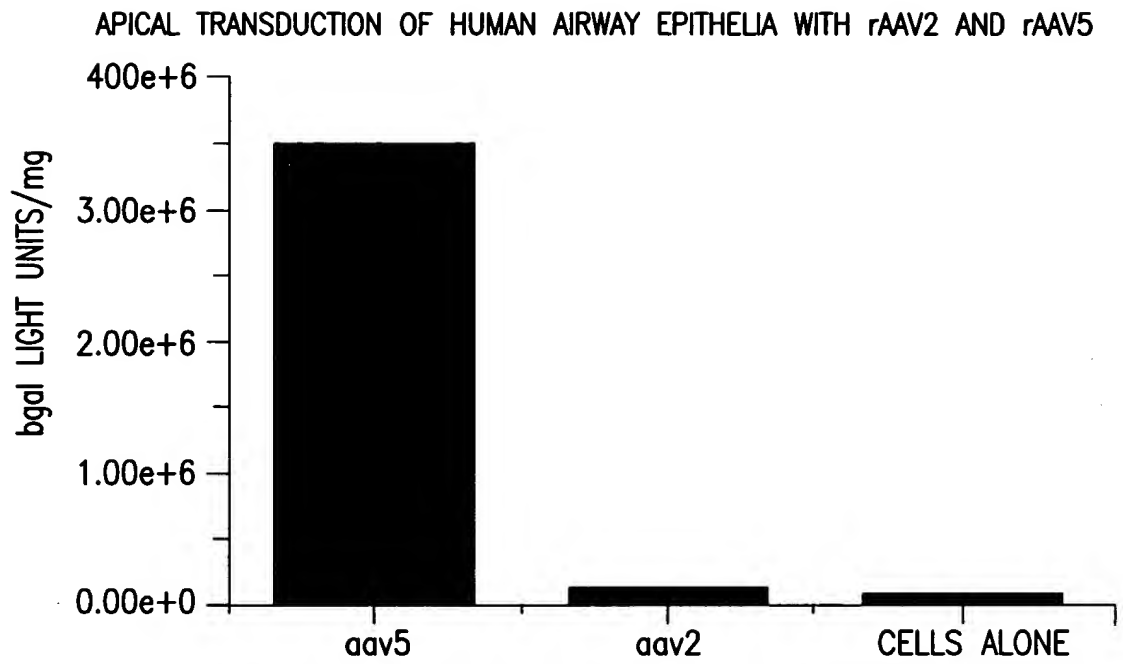


FIG.7

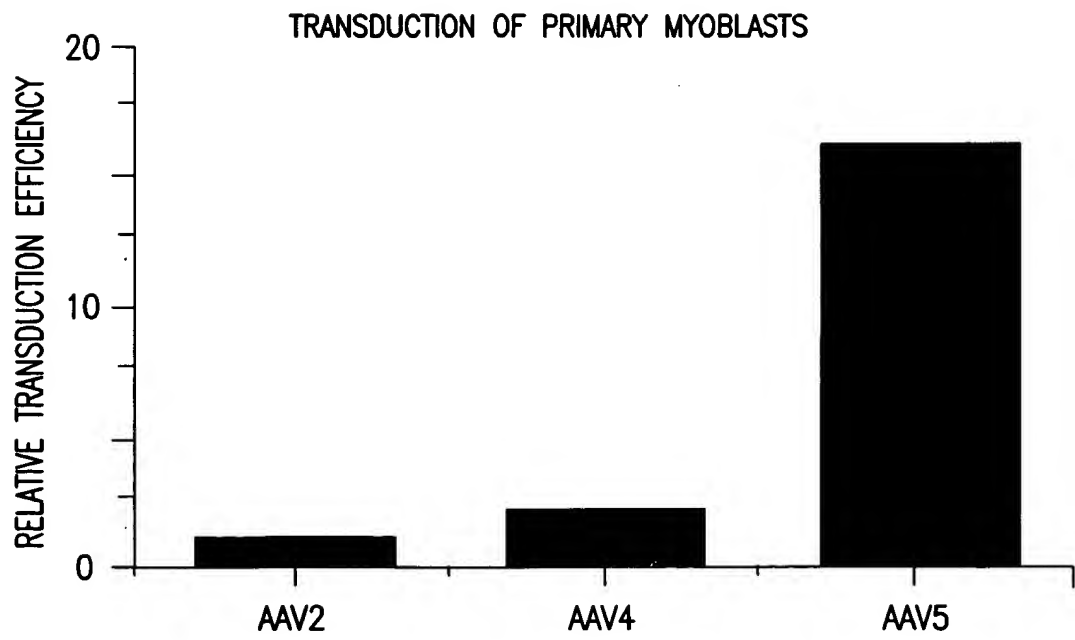


FIG.8

rAAV5 Primary Rat Brain Explant

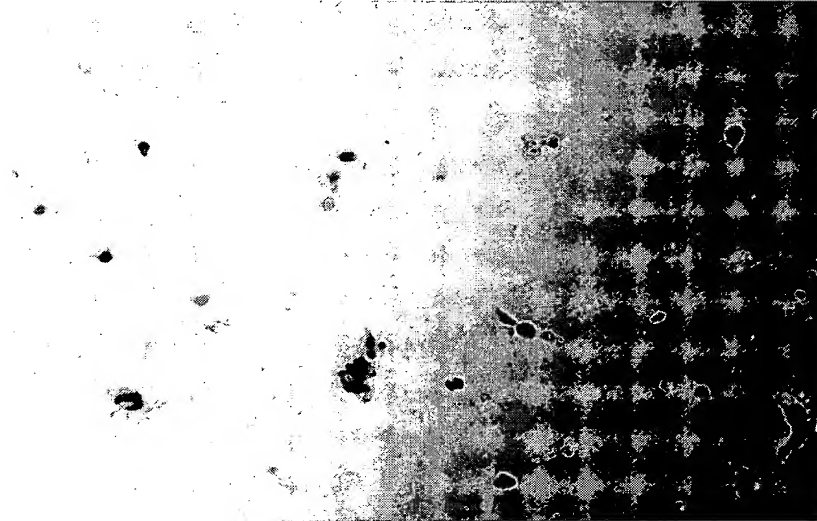


FIG.9

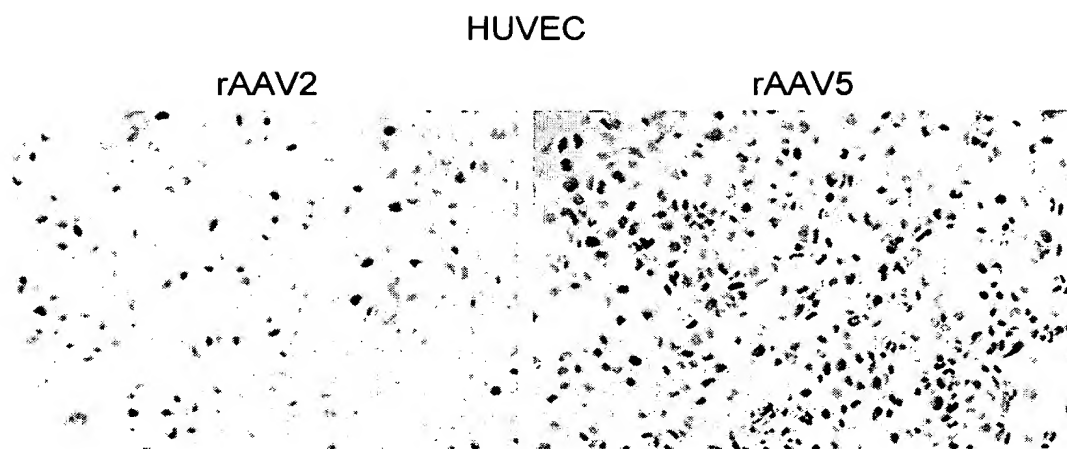


FIG.10

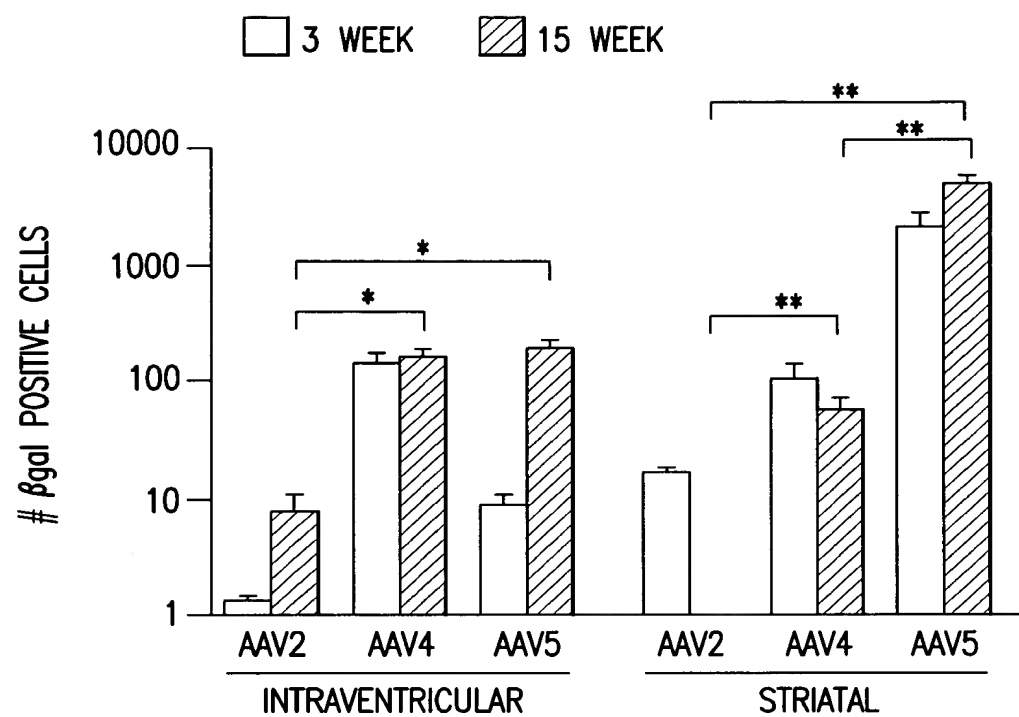


FIG.1 1

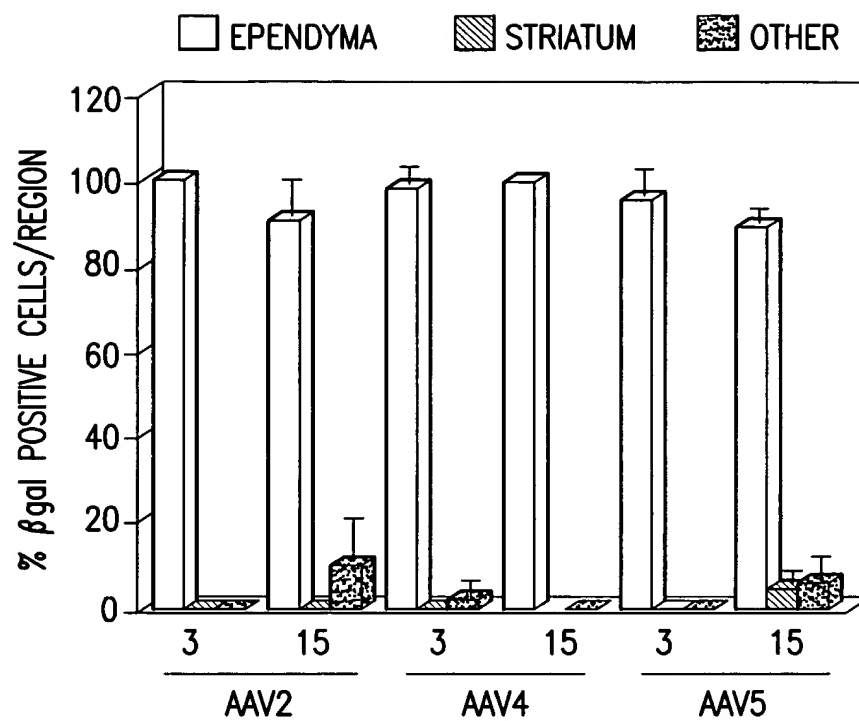


FIG. 12A

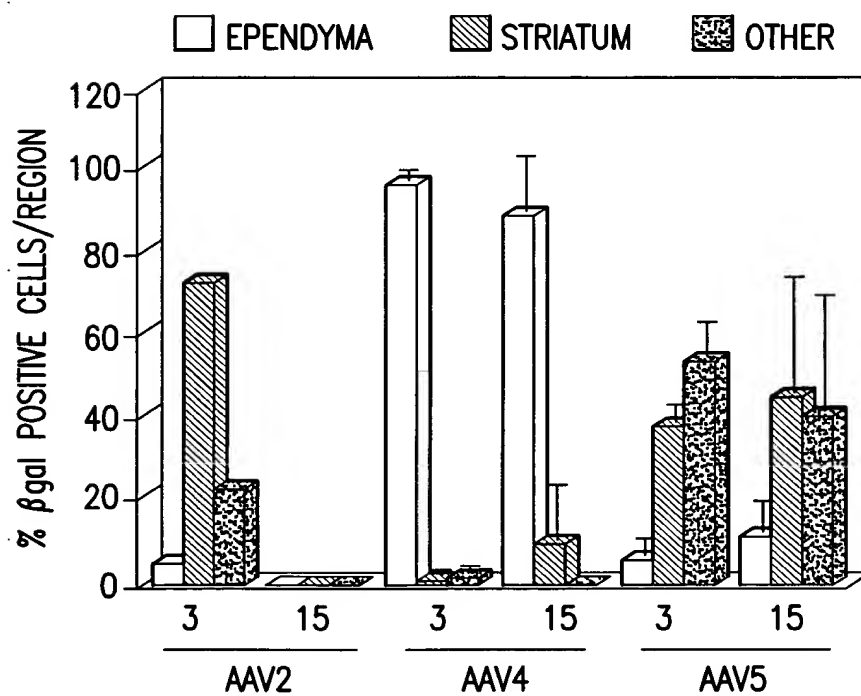


FIG. 12B

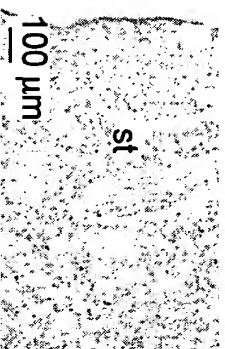


FIG. 13A

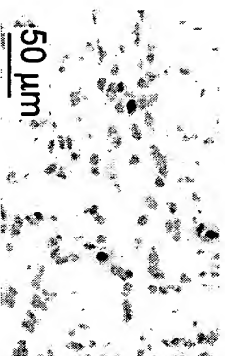


FIG. 13B

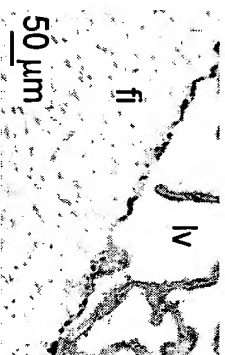


FIG. 13C

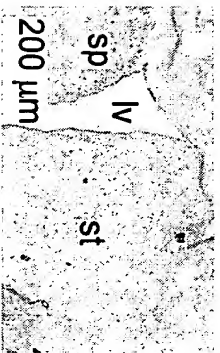


FIG. 13D



FIG. 13E



FIG. 13F

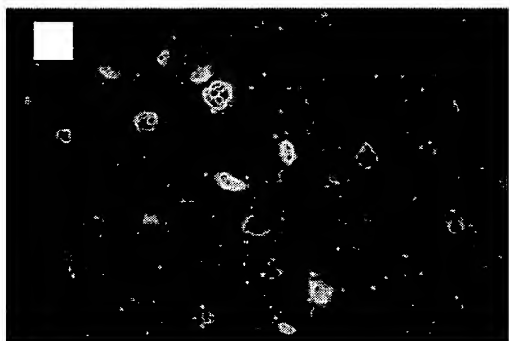


FIG. 14A

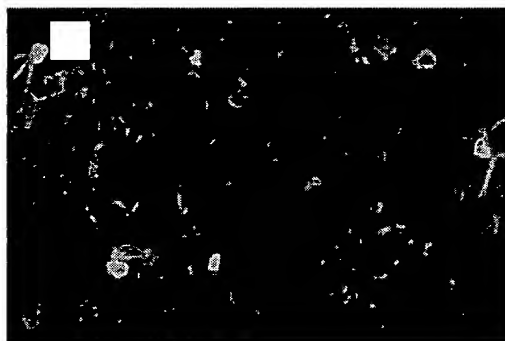


FIG. 14B

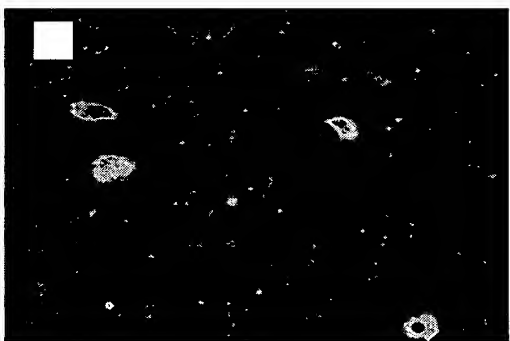


FIG. 14C

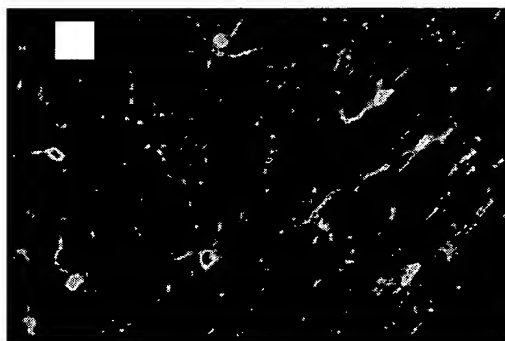


FIG. 14D

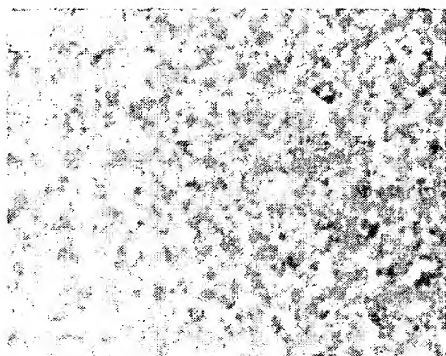


FIG.15A

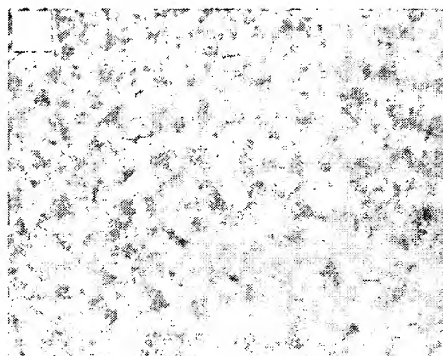


FIG.15B

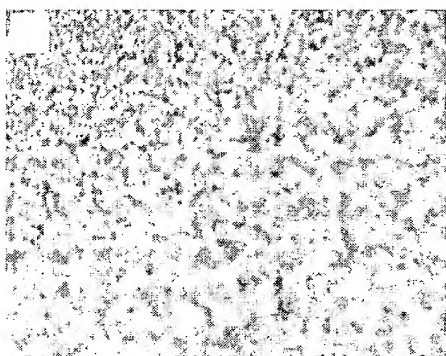


FIG.15C

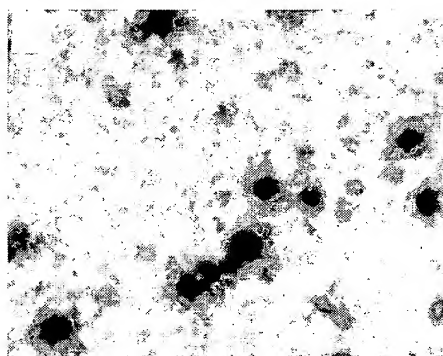


FIG.15D

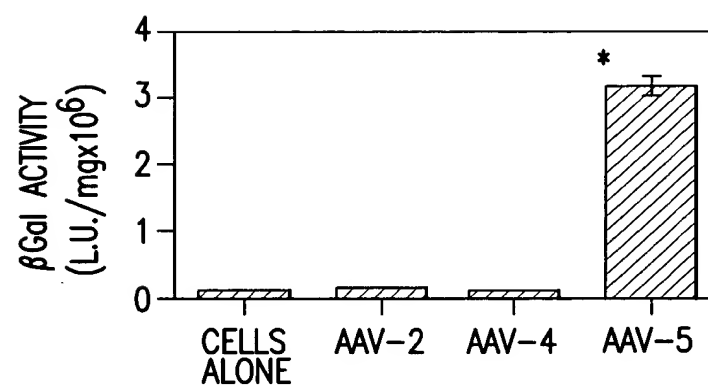


FIG.16A

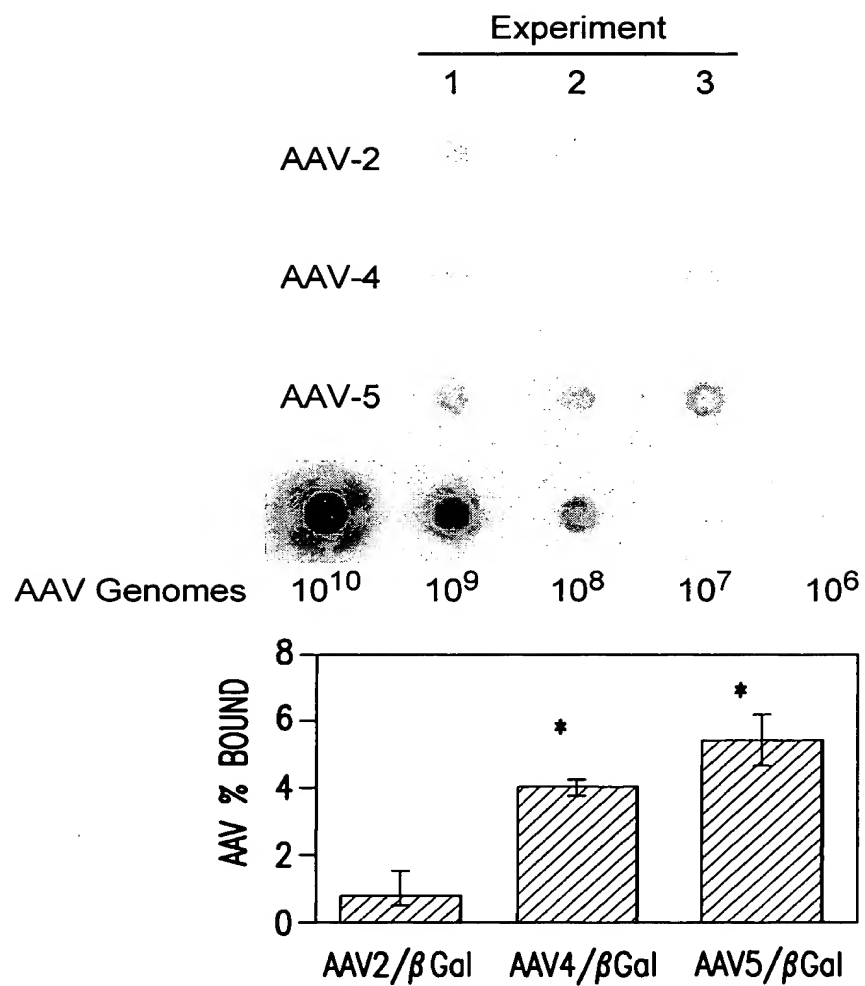


FIG.16B

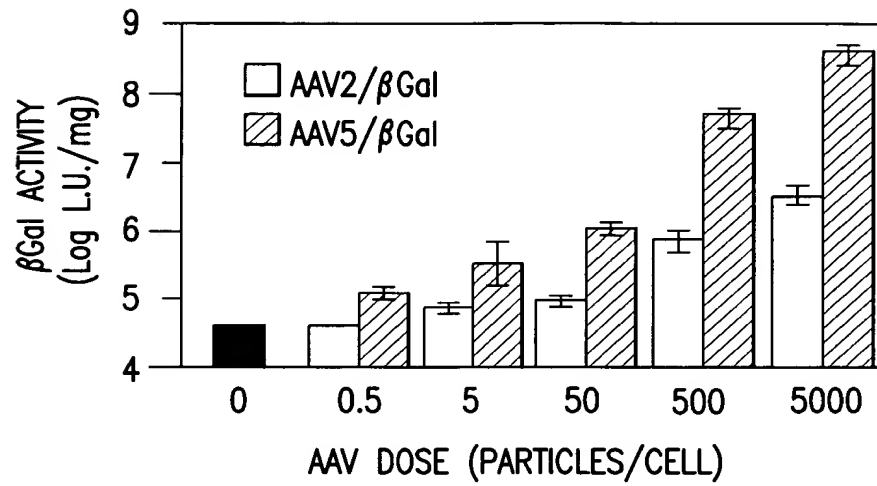


FIG.17

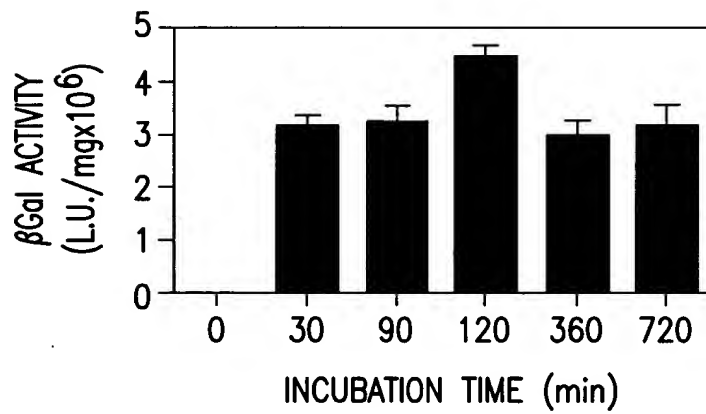


FIG.18

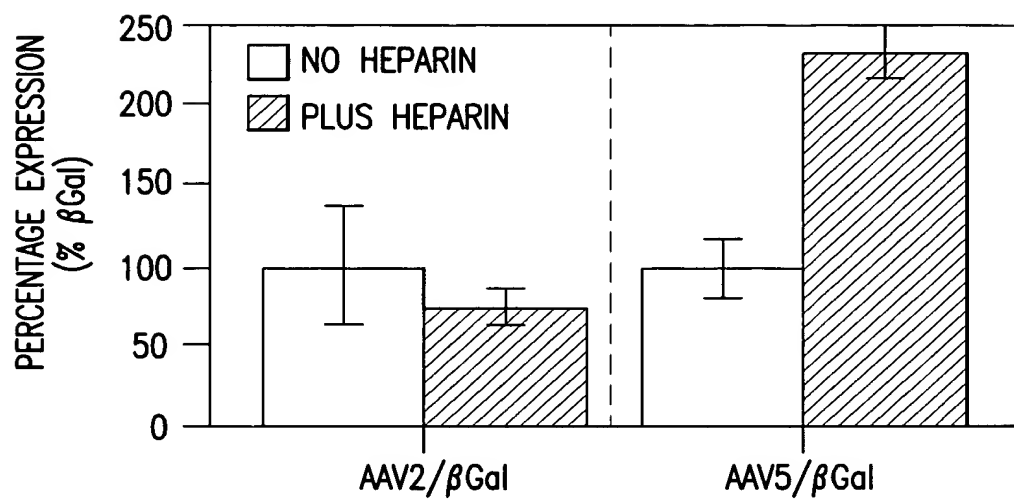


FIG.19A

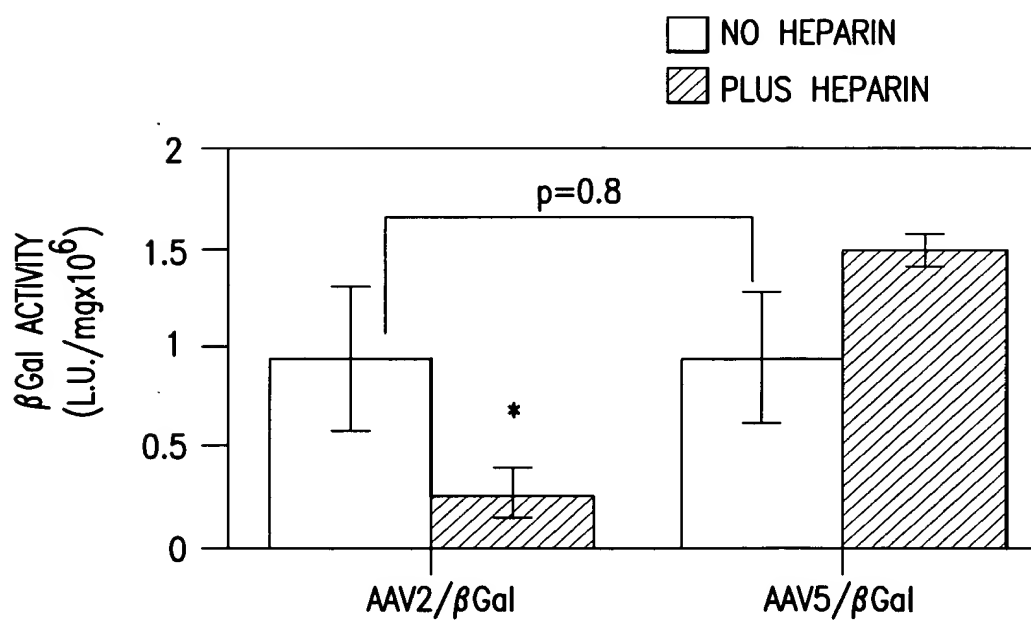


FIG.19B

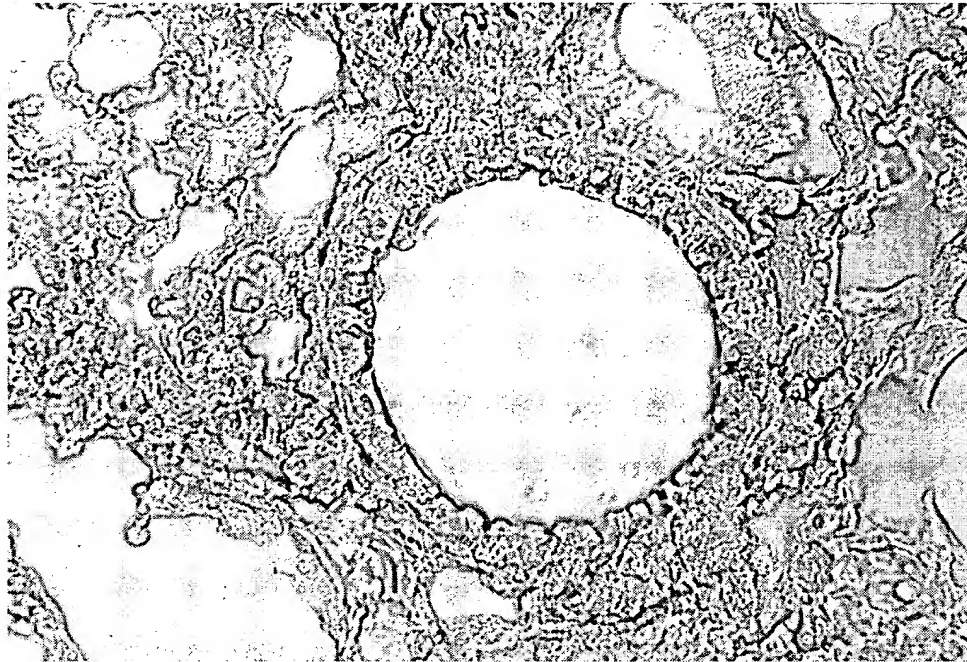


FIG.20A

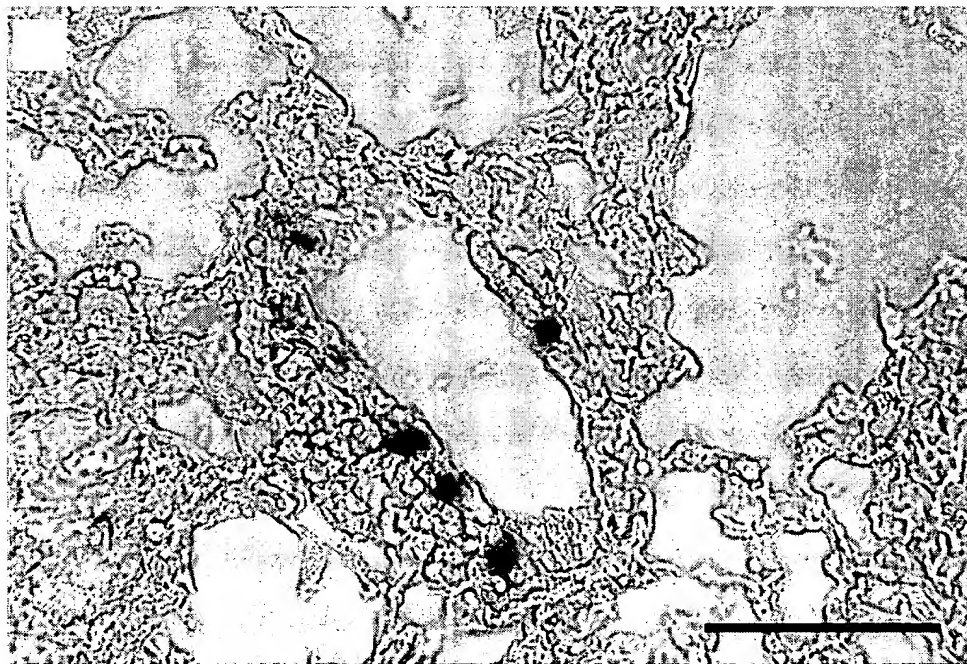


FIG.20B

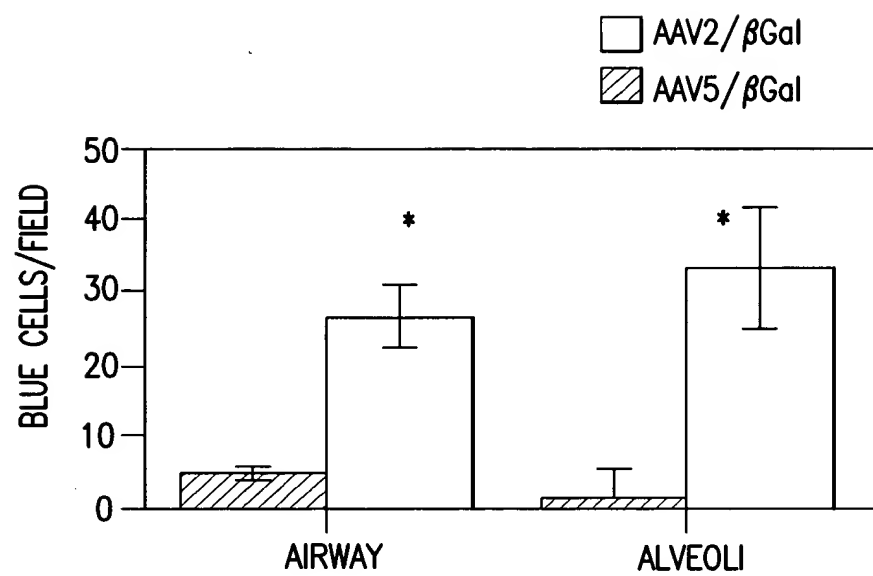


FIG.20C

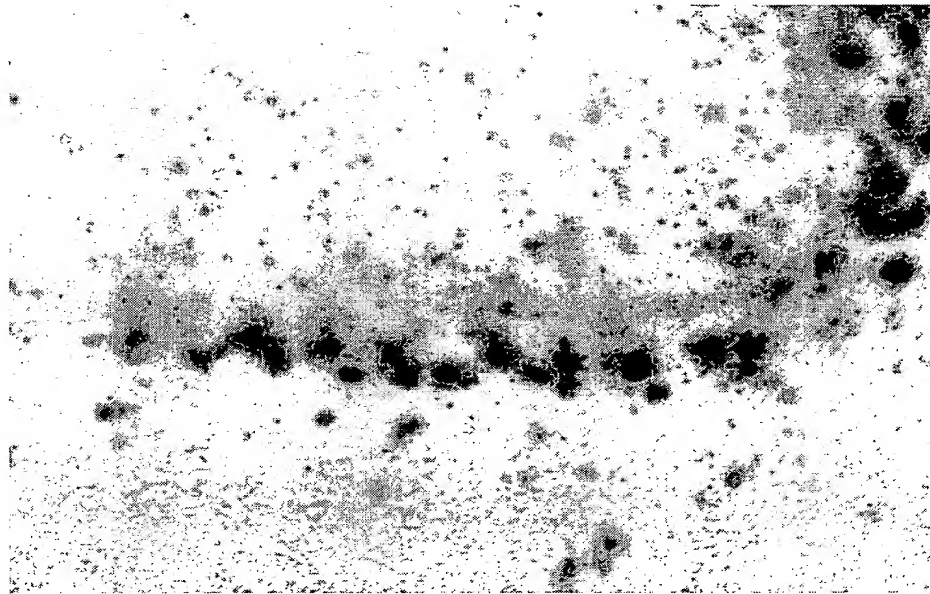


FIG.21

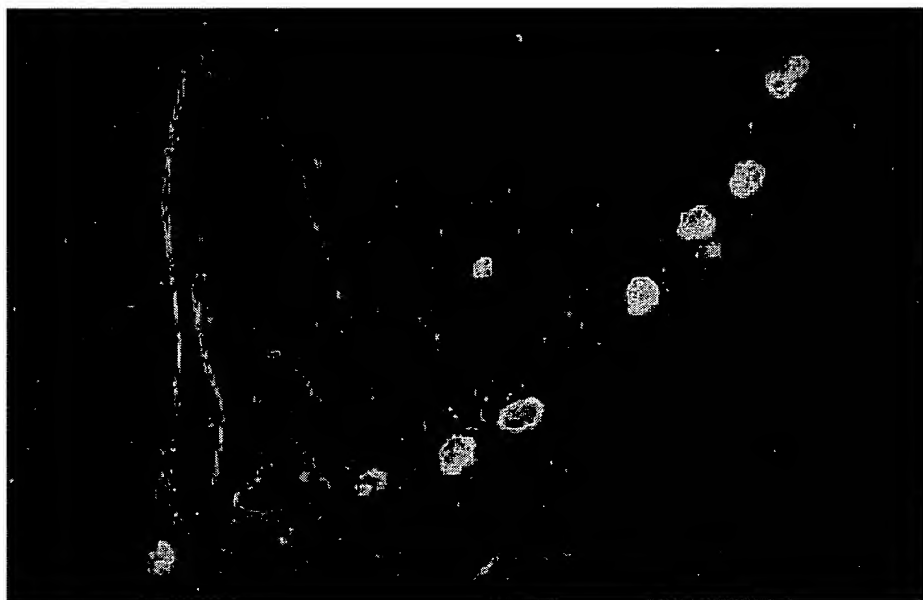


FIG.22

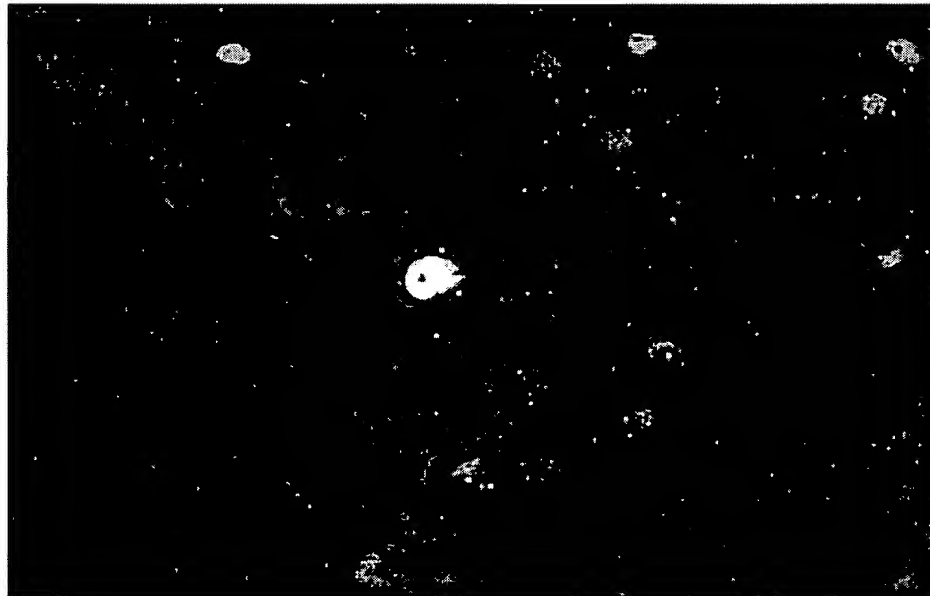


FIG.23

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